

FIGURE 1

1 CCCACGCGTCCGGTCGGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA  
 61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT  
 121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG  
 181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC  
 241 TGAGAGAGTTCTGGGTGTCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA  
 301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG  
 361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA  
 421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCTCTGTCCAAGGC  
 481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT  
 541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTC  
 601 TCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC  
 661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG  
 721 AAAGCAGAGGAAGTGTGTTGTTACCTGGGAACCCCTGGAGGGGGCCTTCCTCATCCGGGAG  
 781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTCTAGTCCGCCTCAGCCGCCCTGCATCCTGG  
 841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACC  
 901 CGCCTCACCTTCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC  
 961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTCAGAGGGCTGGCCCGCTCCCTGGCAAG  
 1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC  
 1081 TCCCTCCTGTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG  
 1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTGGATGATGCCTAG  
 1201 GCCCAAAGGAGAGGCCAAAAGGGAAACCAAGGCTGCACACCTAGAACCCCAATTCAGCCT  
 1261 CCTGGGCACCCCAAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC  
 1321 ATCTAGGGTCCCACCTGTACCCTTGCTCTTCCCTCTCTTAGCCCTTAGAAGTCACCTACT  
 1381 TCCTTCCAGTGCCATGATCCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC  
 1441 AGGGCCAGGGTTCCAAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG  
 1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC  
 1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA  
 1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT  
 1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGATGG  
 1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCTCTAA  
 1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTGGAGACGGAGTCTT  
 1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC  
 1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC  
 1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTCACCACATTGGCC  
 2041 AGGCTGGTGTGCAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG  
 2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCAATTTGTG  
 2161 GCTTACCATTCCTTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT  
 2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA  
 2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC  
 2341 CCTTGATTTCCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC  
 2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTC  
 2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA  
 2521 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAA

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100

## FIGURE 2

1																			M	G
3	S	L	P	S	R	R	K	S	L	P	S	P	S	L	S	S	S	V	Q	G
23	Q	G	P	V	T	M	E	A	E	R	S	K	A	T	A	V	A	L	G	S
43	F	P	A	G	G	P	A	E	L	S	L	R	L	G	E	P	L	T	I	V
63	S	E	D	G	D	W	W	T	V	L	S	E	V	S	G	R	E	Y	N	I
83	P	S	V	H	V	A	K	V	S	H	G	W	L	Y	E	G	L	S	R	E
103	K	A	E	E	L	L	L	L	P	G	N	P	G	G	A	F	L	I	R	E
123	S	Q	T	R	R	G	S	Y	S	L	S	V	R	L	S	R	P	A	S	W
143	D	R	I	R	H	Y	R	I	H	C	L	D	N	G	W	L	Y	I	S	P
163	R	L	T	F	P	S	L	Q	A	L	V	D	H	Y	S	E	L	A	D	D
183	I	C	C	L	L	K	E	P	C	V	L	Q	R	A	G	P	L	P	G	K
203	D	I	P	L	P	V	T	V	Q	R	T	P	L	N	W	K	E	L	D	S
223	S	L	L	F	S	E	A	A	T	G	E	E	S	L	L	S	E	G	L	R
243	E	S	L	S	F	Y	I	S	L	N	D	E	A	V	S	L	D	D	A	*

*(The following are the names of the persons who have been elected to the various offices of the Association, as reported by the Secretary.)*

FIGURE 3A

1 CCCACGCGTCCGGTCGGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA  
 61 GCTCAAAGGGCCCTGGGCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT  
 121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG  
 181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC  
 241 TGAGAGAGTTCTGGGTGTCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA  
 301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCAAGCCTTTG  
 361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA  
 1 M G  
 421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCTCTGTCCAAGGC  
 3 S L P S R R K S L P S P S L S S S V Q G  
 481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT  
 23 Q G P V T M E A E R S K A T A V A L G S  
 541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTC  
 43 F P A G G P A E L S L R L G E P L T I V  
 601 TCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC  
 63 S E D G D W W T V L S E V S G R E Y N I  
 661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG  
 83 P S V H V A K V S H G W L Y E G L S R E  
 721 AAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAG  
 103 K A E E L L L L P G N P G G A F L I R E  
 781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTCTAGTCCGCCTCAGCCGCCCTGCATCCTGG  
 123 S Q T R R G S Y S L S V R L S R P A S W  
 841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG  
 143 D R I R H Y R I H C L D N G W L Y I S P  
 901 CGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC  
 163 R L T F P S L Q A L V D H Y S E L A D D  
 961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCCTGCAGAGGGCTGGCCCGCTCCCTGGCAAG  
 183 I C C L L K E P C V L Q R A G P L P G K  
 1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC  
 203 D I P L P V T V Q R T P L N W K E L D S  
 1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG  
 223 S L L F S E A A T G E E S L L S E G L R  
 1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG  
 243 E S L S F Y I S L N D E A V S L D D A \*  
 1201 GCCCAAAGGAGAGGCCAAAAGGGAAACCAAGGCTGCACACCTAGAACCCCAATTACGCCT  
 1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC  
 1321 ATCTAGGGTCCCACCTGTACCTTGCTCTTCTCTTAGCCCTTAGAAGTCACCTACT  
 1381 TCCTTCCAGTGCCATGATCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC  
 1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG  
 1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC  
 1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA  
 1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100

# FIGURE 3B

1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG  
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCCTCAA  
1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTCTTTTTTTTGTGAGACGGAGTCTT  
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC  
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC  
1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTCACCACATTGGCC  
2041 AGGCTGGTGTGGAACCTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG  
2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCATTTTGTG  
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT  
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA  
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC  
2341 CCTTGATTTCCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC  
2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTC  
2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA  
2522 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAA

1681 1741 1801 1861 1921 1981 2041 2101 2161 2221 2281 2341 2401 2461 2522

FIGURE 4

Homology	Amino acid level	
	Similarity	Identity
human SLAP x mouse SLAP	89.9%	88.0%
human SLAP x human SLAP-2	58.4%	47.4%
mouse SLAP x human SLAP-2	70.0%	58.1%

FIGURE 5

hSLAP-2 1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAE  
: . || |. | . : | . | : | .  
hSLAP 1 ...MGNSMKSTPAPA.....ERLPNPEGLDSDFLAVLSDYPSPDISP

51 LSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLS  
| | | | : : : | | | : | . | | | | | : | | : | | | : | | |  
41 PIFRRGEKLRVISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLG

101 REKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRI RHYRI  
| : | | | | | | | | . | . | : | | | | : | : | | | | | . : : | | | |  
91 RDKAEELLQLPDTKVGSFMIRESETKKGFYSLSVR.....HRQVKHYRI

151 HCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCVLQ RAGPLP  
| | | | | | | | | | : | | . | | | | . | | : | | . | | | . |  
135 FRLPNNWYYISPRLTFQCLEDLVNHYSEVADGLCCVLTTPCLTQSTAAPA

201 GKDIPLPVTVQRTPLNWK...ELDSSLLFSEAATG.EESLLSEGLRESLS  
: | | | | . . . | : | | | | | . | | : | | | | | | | | : :  
185 VRASSSPVTLRQKTVDWRRVSRLQEDPEGTENPLGVDES LFSYGLRESIA

247 FYISLNDEAVSLDDA.....  
| : | | | | . |  
235 SYLSLTSEDNTSFDRKKKSISL MYGGSKRKSSFFSPPYFED

FIGURE 5

```

hSLAP   1 MGNSMKSTPAPAERPLPNPEGLDSDFLAVLSDYSPDISPPIFRRGEKLR
      ||||| | . ||| | . ||| : ||||| | . ||||| | ||||| | ||||| |
mSLAP   1 MGNSMKSTSPPSERPLSSSEGLESDFLAVLTDYSPDISPPIFRRGEKLR

      .           .           .           .
51 VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL
   ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
51 VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL

      .           .           .           .
101 PDTKVGSFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF
    ||| : ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
101 PDTKIGSFMIRES ETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF

      .           .           .           .
151 QCLEDLVNHYSEVADGLCCVLTPCLTQSTAAPAVRAS.....SSPVTLR
    ||||| | ||||| | ||||| | ||||| | . || | | ||||| |
151 QCLEDLVTHYSEVADGLCCVLTPCLAQNI PAPTSHPSPTSPGSPVTLR

      .           .           .           .
196 QKTVDWRRVSRLQEDPEGTENPLGVDES LFSYGLRESIASYLSLTSEDNT
    ||| || : ||||| | || ||| | ||||| | ||||| | ||||| | : |..
201 QKTFDWKRVSRLQEGSEGAENPLRVDES LFSYGLRESIASYLSLTGDDSS

      .           .           .
246 SFDRKKKSISLMYG GSKRKSSFFS SPPYFED 276
    ||||| | : ||| | ||||| | |||. | ||| |
251 SFDRKKKSLSLMYT GSKRKSSFFS SAPQYFED 281

```

**THE UNIVERSITY OF CHICAGO**

## hSLAP-2

**mSLAP**

```

1 MG.SLPSRRKSLPS..PSLSVVQGGPVTMEAERSKATAVALGSFPAGG
  || |: | || | ||| :| :| | || |:|.
1 MGNSMKS..TSPPSERP.LSSS...EG...LE...SDFLAV.LTDYPS..

      .
48 PAELS...LRLGEPLTIVSEDGDWWTVLSEVS.GRE.YNIPSVHVAKVSH
  |:| | || |:|:| || :| .| ||| | || :| |:| |
36 P.DISPPIFRRGEKLRVISDEGGWWKAIS.LSTGRESY.IPGICVARVYH

      .
93 GWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASW
  |||:| | |:| || | |. |:| |:| |:| | | | | |
83 GWLFEGLGRDKAEELLQLPDTKIGSFMIRESETKKGFYSLSVR.HR....

      .
143 DRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCV
  .:| ||| | | | ||||| |:| | |||. | |:| | |.
128 .QVKHYRIFRLPNNWYYISPRLTFQCLEDLVTHYSEVADGLCCVLTTPCL

      .
193 LQR..A.....GPL..PGKDIPLPVTV.QRTPLNWKELDSSLLFSEAATG
  | | | || ||| . |:| .| | . | | | | . |
177 AQNIPAPTSHPSPTSPGS....PVTLRQKT.FDWKRV.SRL..QEGSEG

      .
233 .E.....ESLLSEGLRESLSFYISL.NDEAVSLD
  | ||| | ||||: . |:| |: . | |
219 AENPLRVDESLSFYGLRESIASYLSLTGDDSSSF

```

[illegible]

FIGURE 8

